5 nt | 51 bp

5′
3′
RI | RII

PRE-CLEAVED

FIG. 1A

76 bp
35 bp | 5 bp | 36 bp

5′
3′
ACCGC
TGGCG

FIG. 1A-a

5′
3′
ACXGC
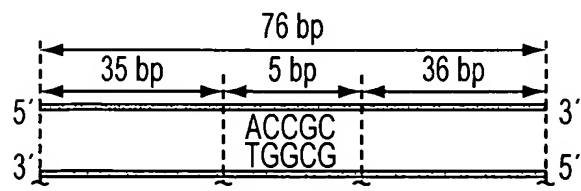TGYCG

FIG. 1A-b
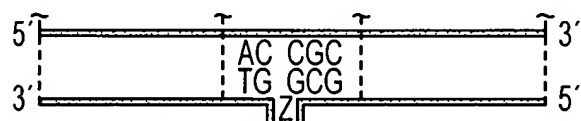
5′
3′
AC CGC
TG GCG
Z

FIG. 1A-c

TARGETS   1 2 3 4 5 6 7 8 9 10
REGULAR   - + - - - - - - - -
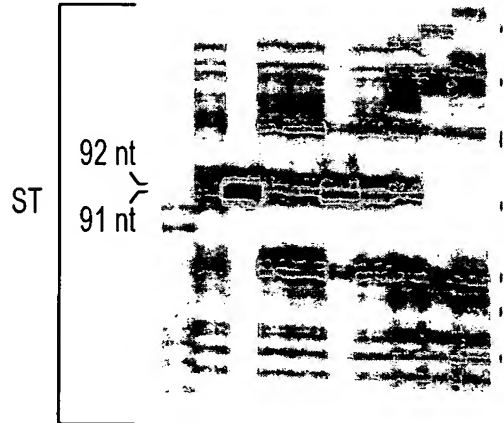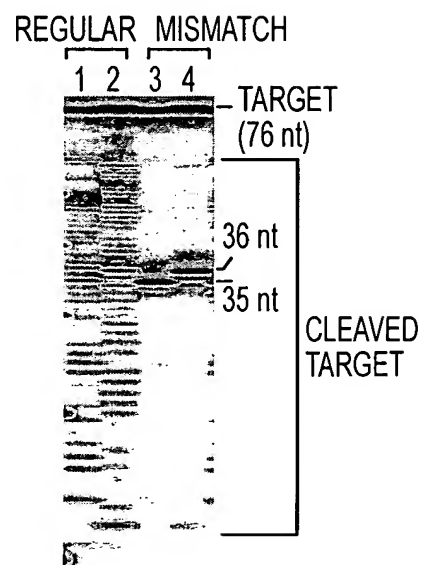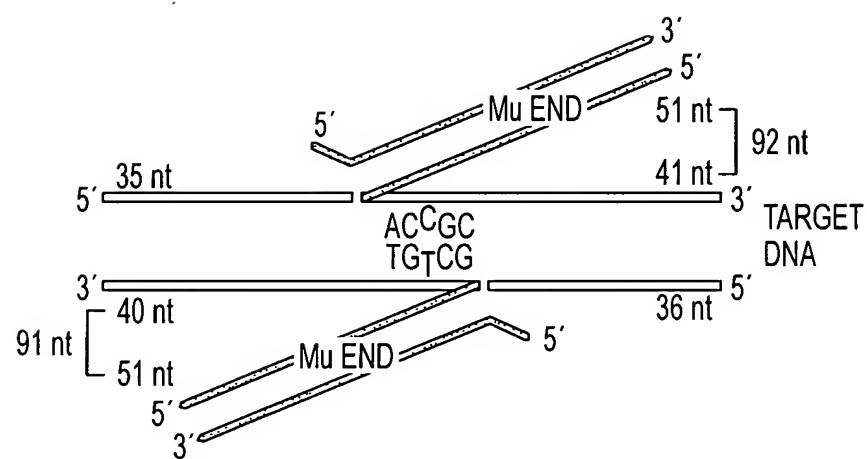MISMATCH   - - C/T - - - - - - -
BULGE   - - - C T G A A²A⁵A¹⁰

ST

92 nt
91 nt

Mu END
(51 nt)

FIG. 1B

REGULAR MISMATCH
1 2   3 4

TARGET
(76 nt)

36 nt
35 nt

CLEAVED
TARGET

FIG. 1C

BEST AVAILABLE COPY

FIG. 1D

FIG. 2A

FIG. 2B

FIG. 3

GENOMIC DNA

CFTR GENE EXON 11
(ALLELE 1; NORMAL)

GTGGA
CACCT

GTGGA
CACCT

CFTR GENE EXON 11
(ALLELE 2; MUTANT)

GTTGA
CAACT

GTTGA
CAACT

PCR

PCR PRODUCTS

GTGGA
CACCT

GT^{T}GA
CA$_C$CT

GT^{G}GA
CA$_A$CT

GTTGA
CAACT

Mu

Mu

TRANSPOSITION PRODUCTS

51 nt
51 nt]102 nt

GT^{T}GA
CA$_C$CT

111 nt [60 nt
51 nt

*

51 nt
51 nt]102 nt

GT^{G}GA
CA$_A$CT

111 nt [60 nt
51 nt
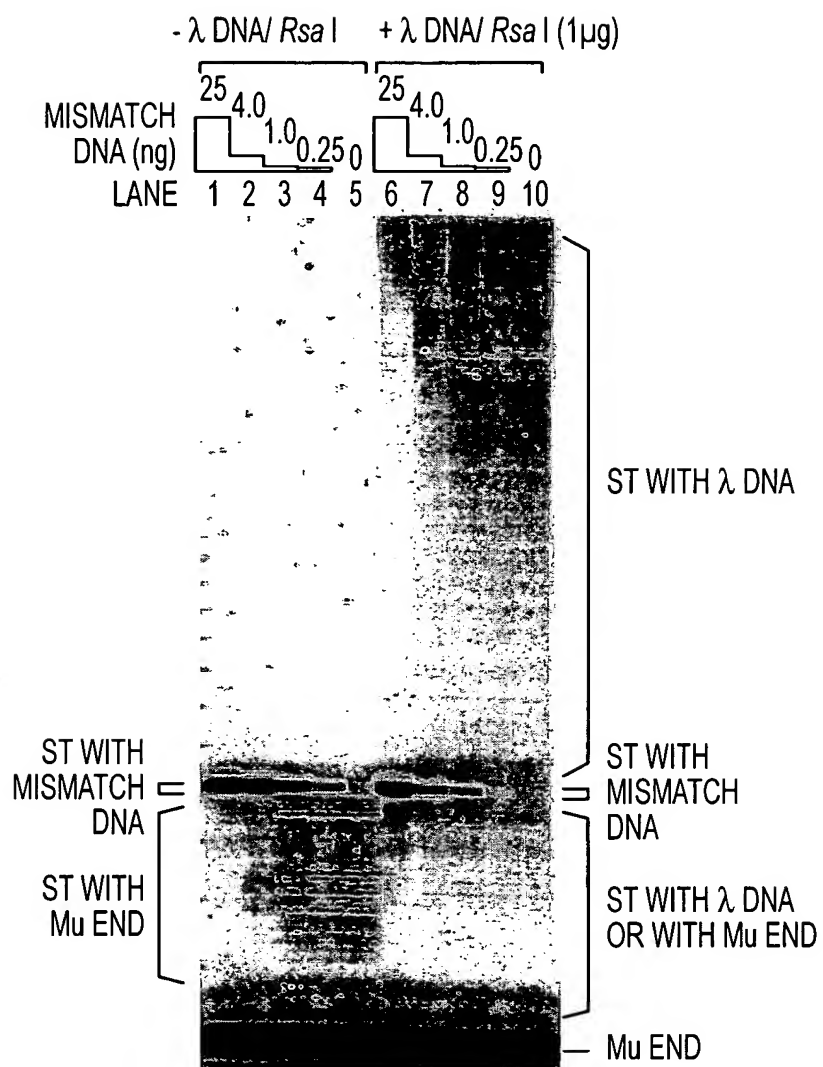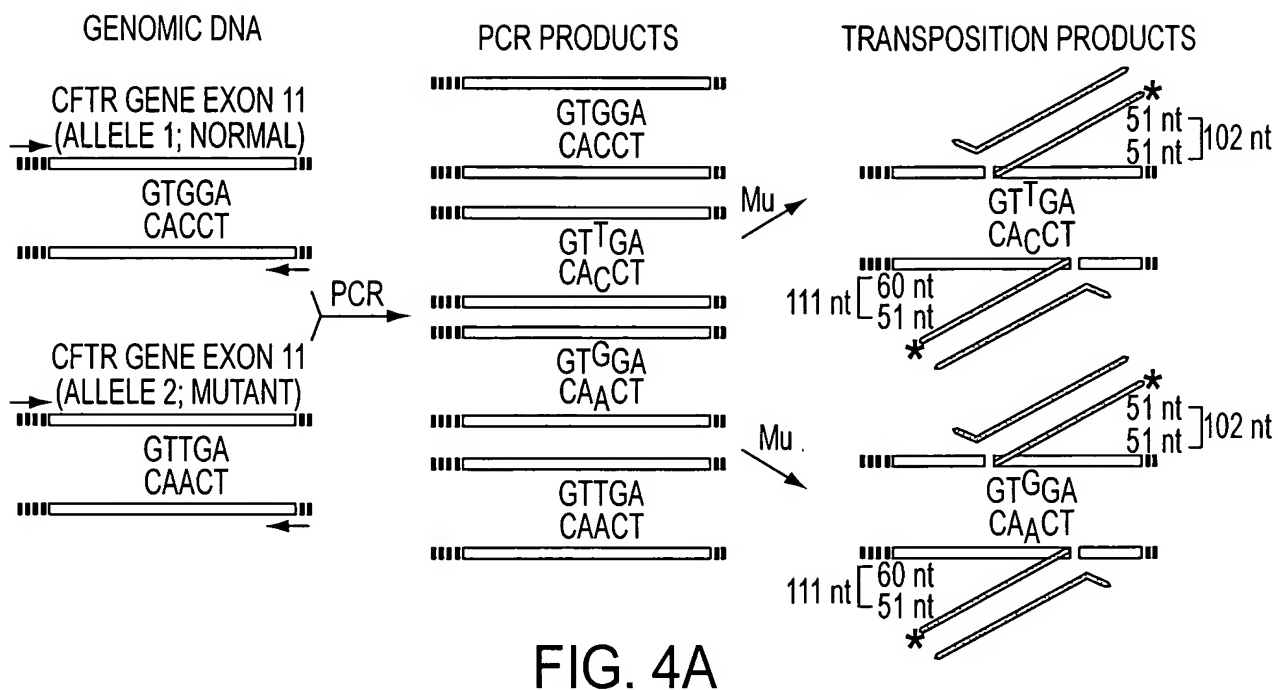
*

FIG. 4A

TEMPLATE
NORMAL (N/N)   + - - + + -
PATIENT (M/M) - + - + - -
SIBLING (N/M) - - + - + -
LANE   1 2 3 4 5 6
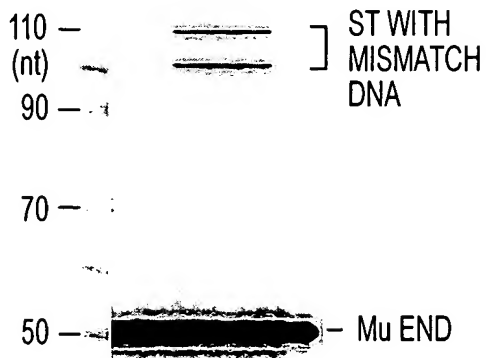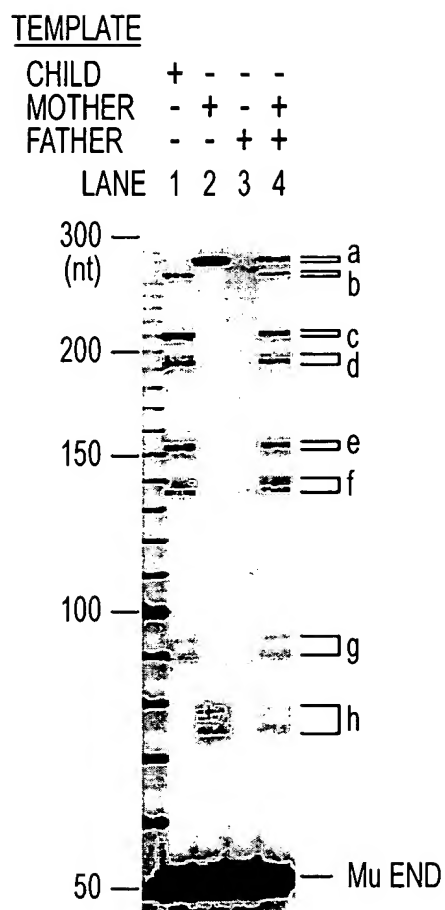
110 —
(nt)

90 —

] ST WITH
MISMATCH
DNA

70 —

50 —   — Mu END

FIG. 4B

FIG. 5